



SEQUENCE LISTING

<110> The Curators of the University of Missouri

<120> PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES

<130> UMO 1521.1

<140> US 09/829,549

<141> 2001-04-10

<150> US 60/195,785

<151> 2000-04-10

<160> 48

<170> PatentIn version 3.0

<210> 1

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<212> PRT

<213> Type 88 filamentous bacteriophage

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<222> (9)..(23)

<223> x=any amino acid encoded by the codon NNK

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<213> Artificial Sequence

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<223> Primer

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Ala Asp Arg Pro Ser Thr Thr Ser Leu  
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Ala Asp Pro Pro Arg Thr Val Ser Thr  
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Ala Asp Arg Pro Ser Met Ser Pro Thr  
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Ala Asp Arg Thr Ser Asn Ala Ser Thr  
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Ser Ala Thr Asp Thr Thr Leu Pro Met Met Thr Ala Ile Arg Ser  
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Met Ser Asn Phe Pro Thr Ser His Ala Pro Cys Pro Val Glu Ile  
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Glu Phe Arg Lys Asn Tyr Pro Ser Ala Ala Pro Leu Ile Pro Arg  
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Pro Xaa Val His Gly Ser Ile Pro Leu Thr Pro Pro Leu Gly Phe  
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Met Ser Asn Phe Pro Thr Ser His Ala Pro Cys Pro Val Xaa Ile  
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Pro Glu Trp Lys Ser Ser Trp Ser Pro Cys Thr Pro Arg Cys Pro  
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Ala Met Ser Arg Trp Leu Arg Pro Arg Glu Xaa Asn Ala Pro Pro  
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<211> 15

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<221> VARIANT

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Thr His Thr Thr Phe Xaa Val Thr Val Xaa Leu His Glu Pro Pro  
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<211> 15

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Ala	Pro	Gln	Cys	His	Pro	His	Leu	Pro	Phe	Asp	Met	Ile	His	Val
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Val	Ala	Ala	Pro	Ser	His	Trp	Leu	Lys	Pro	Ser	Leu	Asp	Cys	Phe
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<211> 15

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Leu	Ile	Phe	Arg	Tyr	Ala	Pro	Pro	Pro	Leu	Phe	Leu	Arg	Pro	Pro
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<211> 36

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36

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			20					25					30			
Ile	Pro	Ala	Asp	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
		35					40					45				
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	50					55					60					
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
65					70				75						80	
Ser	Leu	Glu	Lys	Arg	Leu	Ala	Ala	Gly	Thr	Pro	Ala	Leu	Gly	Asp	Asp	
				85					90					95		
Arg	Gly	Arg	Pro	Trp	Pro	Ala	Ser	Leu	Ala	Ala	Leu	Ala	Leu	Asp	Gly	
			100					105					110			
Lys	Leu	Arg	Thr	Asp	Ser	Asn	Ala	Thr	Ala	Ala	Ala	Ser	Thr	Asp	Phe	
	115						120					125				
Gly	Asn	Ile	Thr	Ser	Ala	Leu	Pro	Ala	Ala	Val	Leu	Tyr	Pro	Ser	Thr	
	130					135					140					
Gly	Asp	Leu	Val	Ala	Leu	Leu	Ser	Ala	Ala	Asn	Ser	Thr	Pro	Gly	Trp	
145					150					155					160	
Pro	Tyr	Thr	Ile	Ala	Phe	Arg	Gly	Arg	Gly	His	Ser	Leu	Met	Gly	Gln	
				165					170					175		
Ala	Phe	Ala	Pro	Gly	Gly	Val	Val	Val	Asn	Met	Ala	Ser	Leu	Gly	Asp	
			180					185					190			
Ala	Ala	Ala	Pro	Pro	Arg	Ile	Asn	Val	Ser	Ala	Asp	Gly	Arg	Tyr	Val	
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Asp	Ala	Gly	Gly	Glu	Gln	Val	Trp	Ile	Asp	Val	Leu	Arg	Ala	Ser	Leu	
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Ala	Arg	Gly	Val	Ala	Pro	Arg	Ser	Trp	Asn	Asp	Tyr	Leu	Tyr	Leu	Thr	
225					230					235					240	
Val	Gly	Gly	Thr	Leu	Ser	Asn	Ala	Gly	Ile	Ser	Gly	Gln	Ala	Phe	Arg	
				245					250					255		
His	Gly	Pro	Gln	Ile	Ser	Asn	Val	Leu	Glu	Met	Asp	Val	Ile	Thr	Gly	
		260						265					270			
His	Gly	Glu	Met	Val	Thr	Cys	Ser	Lys	Gln	Leu	Asn	Ala	Asp	Leu	Phe	
	275						280					285				
Asp	Ala	Val	Leu	Gly	Gly	Leu	Gly	Gln	Phe	Gly	Val	Ile	Thr	Arg	Ala	



290					295					300					
Arg	Ile	Ala	Val	Glu	Pro	Ala	Pro	Ala	Arg	Ala	Arg	Trp	Val	Arg	Phe
305					310					315					320
Val	Tyr	Thr	Asp	Phe	Ala	Ala	Phe	Ser	Ala	Asp	Gln	Glu	Arg	Leu	Thr
				325					330					335	
Ala	Pro	Arg	Pro	Gly	Gly	Gly	Gly	Ala	Ser	Phe	Gly	Pro	Met	Ser	Tyr
			340					345					350		
Val	Glu	Gly	Ser	Val	Phe	Val	Asn	Gln	Ser	Leu	Ala	Thr	Asp	Leu	Ala
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Asn	Thr	Gly	Phe	Phe	Thr	Asp	Ala	Asp	Val	Ala	Arg	Ile	Val	Ala	Leu
	370					375					380				
Ala	Gly	Glu	Arg	Asn	Ala	Thr	Thr	Val	Tyr	Ser	Ile	Glu	Ala	Thr	Leu
385					390					395					400
Asn	Tyr	Asp	Asn	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Val	Asp	Gln	Glu	Leu
				405					410					415	
Ala	Ser	Val	Leu	Gly	Thr	Leu	Ser	Tyr	Val	Glu	Gly	Phe	Ala	Phe	Gln
			420					425					430		
Arg	Asp	Val	Ala	Tyr	Ala	Ala	Phe	Leu	Asp	Arg	Val	His	Gly	Glu	Glu
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	450					455					460				
Asn	Met	Phe	Val	Pro	Arg	Ser	Arg	Ile	Ala	Asp	Phe	Asp	Arg	Gly	Val
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Phe	Lys	Gly	Ile	Leu	Gln	Gly	Thr	Asp	Ile	Val	Gly	Pro	Leu	Ile	Val
				485					490					495	
Tyr	Pro	Leu	Asn	Lys	Ser	Met	Trp	Asp	Asp	Gly	Met	Ser	Ala	Ala	Thr
			500					505					510		
Pro	Ser	Glu	Asp	Val	Phe	Tyr	Ala	Val	Ser	Leu	Leu	Phe	Ser	Ser	Val
		515					520					525			
Ala	Pro	Asn	Asp	Leu	Ala	Arg	Leu	Gln	Glu	Gln	Asn	Arg	Arg	Ile	Leu
		530				535					540				
Arg	Phe	Cys	Asp	Leu	Ala	Gly	Ile	Gln	Tyr	Lys	Thr	Tyr	Leu	Ala	Arg
545					550					555					560
His	Thr	Asp	Arg	Ser	Asp	Trp	Val	Arg	His	Phe	Gly	Ala	Ala	Lys	Trp
				565					570					575	
Asn	Arg	Phe	Val	Glu	Met	Lys	Asn	Lys	Tyr	Asp	Pro	Lys	Arg	Leu	Leu
			580				585						590		
Ser	Pro	Gly	Gln	Asp	Ile	Phe	Asn	Lys	Leu	Ala	Asp	Arg	Pro	Ser	Met

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600

605

Ser Pro Thr  
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# SEQUENCE LISTING

<110> The Curators of the University of Missouri

<120> PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES

<130> UMO 1521.1

<140> US 09/829,549

<141> 2001-04-10

<150> US 60/195,785

<151> 2000-04-10

<160> 48

<170> PatentIn version 3.0

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<212> PRT

<213> Type 88 filamentous bacteriophage

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<223> x=any amino acid encoded by the codon NNK

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agtagcagaa gcctgaaga

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Ala Asp Pro Pro Arg Thr Val Ser Thr  
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Ala Asp Arg Thr Ser Asn Ala Ser Thr  
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<212> PRT  
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<220>  
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<223> Random peptide insert

<400> 10

Ala Asp Lys Ser Tyr Ile Pro Ser Ser  
1 5

<210> 11  
<211> 9  
<212> PRT  
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<220>  
<221> DOMAIN  
<222> (1)..(9)  
<223> Random peptide insert

<400> 11

Ala Val Arg Asn Pro Ser His His Ser  
1 5

<210> 12  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(9)  
<223> Random peptide insert

<400> 12

Ala Asp Pro Thr Pro Arg Gly His Ser  
1 5

<210> 13  
<211> 9  
<212> PRT  
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<220>  
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<222> (1)..(9)  
<223> Random peptide insert

<400> 13

Ala Asp Pro Thr Arg Gln Pro His Ser

1 5

<210> 14  
<211> 9  
<212> PRT  
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<220>  
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<222> (1)..(9)  
<223> Random peptide insert

<400> 14

Ala Glu His Gln Asn Ser Ala Gly Pro  
1 5

<210> 15  
<211> 10  
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<220>  
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<222> (1)..(10)  
<223> Random peptide insert

<400> 15

Ala Asp Ala Arg Ser Ala Gly Ala Ile Ser  
1 5 10

<210> 16  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
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<222> (1)..(9)  
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<400> 16

Ala Asp Ser Lys Asn Ala Gly Pro Met  
1 5

<210> 17  
<211> 9  
<212> PRT  
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<220>  
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<222> (1)..(9)  
<223> Random peptide insert

<400> 17

Ala Glu Thr Lys Phe Ser Gly Ser Ala  
1 5

<210> 18  
<211> 9  
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<220>  
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<222> (1)..(9)  
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<400> 18

Ala Asp Pro Lys Gly Ser Gly Val Thr  
1 5

<210> 19  
<211> 9  
<212> PRT  
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<220>  
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<222> (1)..(9)  
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<400> 19

Ala Gly Leu Thr Ser Pro Asn Asp Met  
1 5

<210> 20  
<211> 9  
<212> PRT  
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<220>  
<221> DOMAIN  
<222> (1)..(9)  
<223> Random peptide insert

<400> 20

Ala Asp Ile Thr Asp Pro Met Gly Ala  
1 5



<210> 21  
<211> 9  
<212> PRT  
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<220>  
<221> DOMAIN  
<222> (1)..(9)  
<223> Random peptide insert

<400> 21

Ala Val Gly Thr His Thr Pro Asp Ser  
1 5

<210> 22  
<211> 9  
<212> PRT  
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<220>  
<221> DOMAIN  
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<400> 22

Ala Val Ser Pro Asn Val His Asp Gly  
1 5

<210> 23  
<211> 15  
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<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 23

Val Ala Ala Phe Ser Leu Val Trp Ala Thr His Leu Met Leu Ser  
1 5 10 15

<210> 24  
<211> 15  
<212> PRT  
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<220>  
<221> DOMAIN  
<222> (1)..(15)  
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<400> 24

Leu Thr Arg Cys Leu Val Ser Thr Glu Met Ala Ala Arg Arg Pro  
1 5 10 15

<210> 25  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
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<400> 25

Ser Ala Pro Tyr Leu Pro Tyr Phe Asp Leu Leu His Phe Pro Ile  
1 5 10 15

<210> 26  
<211> 15  
<212> PRT  
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<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
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<223> x=unknown amino acid

<400> 26

Pro Ser Ser Tyr Glu Ala Ser Arg Arg Pro Glu His Trp Xaa Phe  
1 5 10 15

<210> 27  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 27

Ser Ala Thr Asp Thr Thr Leu Pro Met Met Thr Ala Ile Arg Ser  
1 5 10 15

<210> 28  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (9)..(9)  
<223> x=unknown amino acid

<400> 28

Thr Arg Leu Ser Pro Met Glu Ser Xaa Ala Met Leu Leu Ala Pro  
1 5 10 15

<210> 29  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 29

Leu Leu Pro Val Ser Pro Pro Phe Ala Pro Asn Ala Ser Ser Thr  
1 5 10 15

<210> 30  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 30

Met Ser Asn Phe Pro Thr Ser His Ala Pro Cys Pro Val Glu Ile  
1 5 10 15

<210> 31  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 31

Glu Phe Arg Lys Asn Tyr Pro Ser Ala Ala Pro Leu Ile Pro Arg  
1 5 10 15

<210> 32  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (2)..(2)  
<223> x=unknown amino acid

<400> 32

Pro Xaa Val His Gly Ser Ile Pro Leu Thr Pro Pro Leu Gly Phe  
1 5 10 15

<210> 33  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (3)..(3)  
<223> x=unknown amino acid

<400> 33

Leu Phe Xaa Cys Tyr Pro Pro Cys Thr Tyr Ser Tyr Cys Leu Ser  
1 5 10 15

<210> 34  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (14)..(14)  
<223> x=unknown amino acid

<400> 34

Met Ser Asn Phe Pro Thr Ser His Ala Pro Cys Pro Val Xaa Ile  
1 5 10 15

<210> 35  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 35

Pro Glu Trp Lys Ser Ser Trp Ser Pro Cys Thr Pro Arg Cys Pro  
1 5 10 15

<210> 36  
<211> 15  
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<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (11)..(11)  
<223> x=unknown amino acid

<400> 36

Ala Met Ser Arg Trp Leu Arg Pro Arg Glu Xaa Asn Ala Pro Pro  
1 5 10 15

<210> 37

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<222> (1)..(15)

<223> Random peptide insert

<220>

<221> VARIANT

<222> (6)..(6)

<223> x=unknown amino acid

<220>

<221> VARIANT

<222> (10)..(10)

<223> x=unknown amino acid

<400> 37

Thr His Thr Thr Phe Xaa Val Thr Val Xaa Leu His Glu Pro Pro  
1 5 10 15

<210> 38

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<222> (1)..(15)

<223> Random peptide insert

<400> 38

Met Thr Ser Pro Arg Asn Ser Gln Leu Ile Val Pro Phe Cys Leu  
1 5 10 15

<210> 39

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 39

Pro	Thr	Leu	Gly	Arg	Phe	Asn	Arg	Pro	Ser	Cys	Ser	Ile	Ile	Val
1				5					10					15

<210> 40  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 40

Ala	Pro	Gln	Cys	His	Pro	His	Leu	Pro	Phe	Asp	Met	Ile	His	Val
1				5					10					15

<210> 41  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<220>  
<221> VARIANT  
<222> (12)..(12)  
<223> x=unknown amino acid

<400> 41

Asn	His	Asn	Ser	Leu	Pro	Ala	Gln	Tyr	Leu	Val	Xaa	Ile	Leu	Arg
1				5					10					15

<210> 42  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> DOMAIN  
<222> (1)..(15)  
<223> Random peptide insert

<400> 42

Asp	Gln	Pro	Cys	Thr	Pro	Ser	Pro	Asp	Val	Ser	Phe	Tyr	Arg	Ser
1				5					10					15

<210> 43

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<222> (1)..(15)

<223> Random peptide insert

<400> 43

Val	Ala	Ala	Pro	Ser	His	Trp	Leu	Lys	Pro	Ser	Leu	Asp	Cys	Phe
1				5					10					15

<210> 44

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<222> (1)..(15)

<223> Random peptide insert

<400> 44

Asn	Pro	Leu	Tyr	Lys	Asn	Pro	Pro	Pro	Arg	Val	Ala	Met	Cys	Leu
1				5					10					15

<210> 45

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> DOMAIN

<222> (1)..(15)

<223> Random peptide insert

<400> 45

Leu	Ile	Phe	Arg	Tyr	Ala	Pro	Pro	Pro	Leu	Phe	Leu	Arg	Pro	Pro
1				5					10					15

<210> 46

<211> 36



<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223> + strand of DNA encoding random peptide Pc 87

<400> 46  
agctagcaga tagaccatca atgtcaccaa catagt 36

<210> 47  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223> - strand of DNA encoding peptide Pc 87

<400> 47  
ctagactatg ttggtgacat tgatggtcta tctgct 36

<210> 48  
<211> 611  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1)..(85)  
<223> Mat-alpha secretory sequence

<220>  
<221> DOMAIN  
<222> (86)..(600)  
<223> Cytokinin oxidase 1

<220>  
<221> DOMAIN  
<222> (601)..(602)  
<223> Linker

<220>  
<221> DOMAIN  
<222> (603)..(611)  
<223> Random peptide Pc 87

<400> 48

Met	Arg	Phe	Pro	Ser	Ile	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	
1				5					10					15		
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	
			20					25					30			
Ile	Pro	Ala	Asp	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	
		35					40					45				
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	
	50					55					60					
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	
65					70				75						80	
Ser	Leu	Glu	Lys	Arg	Leu	Ala	Ala	Gly	Thr	Pro	Ala	Leu	Gly	Asp	Asp	
				85					90					95		
Arg	Gly	Arg	Pro	Trp	Pro	Ala	Ser	Leu	Ala	Ala	Leu	Ala	Leu	Asp	Gly	
			100					105					110			
Lys	Leu	Arg	Thr	Asp	Ser	Asn	Ala	Thr	Ala	Ala	Ala	Ser	Thr	Asp	Phe	
	115						120					125				
Gly	Asn	Ile	Thr	Ser	Ala	Leu	Pro	Ala	Ala	Val	Leu	Tyr	Pro	Ser	Thr	
	130					135					140					
Gly	Asp	Leu	Val	Ala	Leu	Leu	Ser	Ala	Ala	Asn	Ser	Thr	Pro	Gly	Trp	
145					150					155					160	
Pro	Tyr	Thr	Ile	Ala	Phe	Arg	Gly	Arg	Gly	His	Ser	Leu	Met	Gly	Gln	
				165					170					175		
Ala	Phe	Ala	Pro	Gly	Gly	Val	Val	Val	Asn	Met	Ala	Ser	Leu	Gly	Asp	
			180					185					190			
Ala	Ala	Ala	Pro	Pro	Arg	Ile	Asn	Val	Ser	Ala	Asp	Gly	Arg	Tyr	Val	
		195					200					205				
Asp	Ala	Gly	Gly	Glu	Gln	Val	Trp	Ile	Asp	Val	Leu	Arg	Ala	Ser	Leu	
	210					215					220					
Ala	Arg	Gly	Val	Ala	Pro	Arg	Ser	Trp	Asn	Asp	Tyr	Leu	Tyr	Leu	Thr	
225					230					235					240	
Val	Gly	Gly	Thr	Leu	Ser	Asn	Ala	Gly	Ile	Ser	Gly	Gln	Ala	Phe	Arg	
				245					250					255		
His	Gly	Pro	Gln	Ile	Ser	Asn	Val	Leu	Glu	Met	Asp	Val	Ile	Thr	Gly	
		260						265					270			
His	Gly	Glu	Met	Val	Thr	Cys	Ser	Lys	Gln	Leu	Asn	Ala	Asp	Leu	Phe	
		275					280					285				
Asp	Ala	Val	Leu	Gly	Gly	Leu	Gly	Gln	Phe	Gly	Val	Ile	Thr	Arg	Ala	

290					295					300					
Arg	Ile	Ala	Val	Glu	Pro	Ala	Pro	Ala	Arg	Ala	Arg	Trp	Val	Arg	Phe
305					310					315					320
Val	Tyr	Thr	Asp	Phe	Ala	Ala	Phe	Ser	Ala	Asp	Gln	Glu	Arg	Leu	Thr
				325					330					335	
Ala	Pro	Arg	Pro	Gly	Gly	Gly	Gly	Ala	Ser	Phe	Gly	Pro	Met	Ser	Tyr
			340					345					350		
Val	Glu	Gly	Ser	Val	Phe	Val	Asn	Gln	Ser	Leu	Ala	Thr	Asp	Leu	Ala
		355					360					365			
Asn	Thr	Gly	Phe	Phe	Thr	Asp	Ala	Asp	Val	Ala	Arg	Ile	Val	Ala	Leu
	370					375					380				
Ala	Gly	Glu	Arg	Asn	Ala	Thr	Thr	Val	Tyr	Ser	Ile	Glu	Ala	Thr	Leu
385					390					395					400
Asn	Tyr	Asp	Asn	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Val	Asp	Gln	Glu	Leu
				405					410					415	
Ala	Ser	Val	Leu	Gly	Thr	Leu	Ser	Tyr	Val	Glu	Gly	Phe	Ala	Phe	Gln
			420					425					430		
Arg	Asp	Val	Ala	Tyr	Ala	Ala	Phe	Leu	Asp	Arg	Val	His	Gly	Glu	Glu
		435					440					445			
Val	Ala	Leu	Asn	Lys	Leu	Gly	Leu	Trp	Arg	Val	Pro	His	Pro	Trp	Leu
	450					455					460				
Asn	Met	Phe	Val	Pro	Arg	Ser	Arg	Ile	Ala	Asp	Phe	Asp	Arg	Gly	Val
465					470					475					480
Phe	Lys	Gly	Ile	Leu	Gln	Gly	Thr	Asp	Ile	Val	Gly	Pro	Leu	Ile	Val
				485					490					495	
Tyr	Pro	Leu	Asn	Lys	Ser	Met	Trp	Asp	Asp	Gly	Met	Ser	Ala	Ala	Thr
			500					505					510		
Pro	Ser	Glu	Asp	Val	Phe	Tyr	Ala	Val	Ser	Leu	Leu	Phe	Ser	Ser	Val
		515					520					525			
Ala	Pro	Asn	Asp	Leu	Ala	Arg	Leu	Gln	Glu	Gln	Asn	Arg	Arg	Ile	Leu
	530					535					540				
Arg	Phe	Cys	Asp	Leu	Ala	Gly	Ile	Gln	Tyr	Lys	Thr	Tyr	Leu	Ala	Arg
545					550					555					560
His	Thr	Asp	Arg	Ser	Asp	Trp	Val	Arg	His	Phe	Gly	Ala	Ala	Lys	Trp
				565					570					575	
Asn	Arg	Phe	Val	Glu	Met	Lys	Asn	Lys	Tyr	Asp	Pro	Lys	Arg	Leu	Leu
			580					585					590		
Ser	Pro	Gly	Gln	Asp	Ile	Phe	Asn	Lys	Leu	Ala	Asp	Arg	Pro	Ser	Met

595

600

605

Ser Pro Thr  
610